

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/537,061

Source: pg 10

Date Processed by STIC: 6/13/05

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RAW SEQUENCE LISTING

DATE: 06/13/2005

PATENT APPLICATION: US/10/537,061

TIME: 09:40:09

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\06132005\J537061.raw

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3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
4   REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
5   HUMAN SERVICES
6   SLOAN-KETTERING INSTITUTE FOR CANCER RESEARCH
7   Pastan, Ira
8   Onda, Masanori
9   Cheung, Nai-Kong
11 <120> TITLE OF INVENTION: IN-VIVO CYTOTOXIC ACTIVITIES OF RECOMBINANT IMMUNOTOXIN 8H9
12   (FV)-PE38 AGAINST BREAST CANCER, OSTEOCARCINOMA AND NEUROBLASTOMA
14 <130> FILE REFERENCE: 4239-67287-05
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/537,061
C--> 16 <141> CURRENT FILING DATE: 2005-06-01
16 <150> PRIOR APPLICATION NUMBER: PCT/US03/038227
17 <151> PRIOR FILING DATE: 2003-12-01
19 <150> PRIOR APPLICATION NUMBER: US 60/430,305
20 <151> PRIOR FILING DATE: 2002-12-02
22 <160> NUMBER OF SEQ ID NOS: 17
24 <170> SOFTWARE: PatentIn version 3.2
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 731
28 <212> TYPE: DNA
29 <213> ORGANISM: Mus musculus
31 <400> SEQUENCE: 1
32 caggtcaaac tgcagcagtc tggggctgaa ctggttaaagc ctggggcttc agtgaaattg      60
34 tcctgcaagg cttctggcta caccttcaca aactatgata taaactgggt gaggcagagg      120
36 cctgaacagg gacttgagtg gattggatgg atttttctct gagatggtag tactcaatac      180
38 aatgagaagt tcaagggcaa ggccacactg actacagaca catcctccag cacagcctac      240
40 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagacagact      300
42 acggctacct ggtttgctta ctggggccaa gggaccacgg tcaccgtctc ctcagatgga      360
44 ggcggttcag gcggaggtgg ctctggcggt ggcggtatcg acatcgagct cactcagtct      420
46 ccaaccaccc tgtctgtgac tccaggagat agagtctctc ttctctgcag ggccagccag      480
48 agtattagcg actacttaca ctggtaccaa caaaaatcac atgagtctcc aaggcttctc      540
50 atcaaatatg cttcccaatc catctctggg atcccctcca ggttcagtgg cagtggatca      600
52 ggtcagatt tactctcag tatcaacagt gtggaacctg aagatgttgg agtgattac      660
54 tgtcaaaatg gtcacagctt tccgctcacg ttcggtgctg ggaccaagct ggagctgaaa      720
56 caggcgccg c                                     731
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 243
61 <212> TYPE: PRT
62 <213> ORGANISM: Mus musculus
64 <400> SEQUENCE: 2
66 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
67 1          5          10          15

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70 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
71          20          25          30
74 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
75          35          40          45
78 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
79          50          55          60
82 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Thr Ala Tyr
83 65          70          75          80
86 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
87          85          90          95
90 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
91          100         105         110
94 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Ser
95          115         120         125
98 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
99          130         135         140
102 Ser Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln
103 145          150         155         160
106 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
107          165         170         175
110 Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
111          180         185         190
114 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
115          195         200         205
118 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
119          210         215         220
122 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
123 225          230         235         240
126 Gln Ala Ala
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 243
132 <212> TYPE: PRT
133 <213> ORGANISM: Mus musculus
135 <400> SEQUENCE: 3
137 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala
138 1          5          10          15
141 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
142          20          25          30
145 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
146          35          40          45
149 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
150          50          55          60
153 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Thr Ala Tyr
154 65          70          75          80
157 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
158          85          90          95
161 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
162          100         105         110
165 Thr Val Thr Val Ser Ser Asp Gly Gly Gly Ser Gly Gly Gly Ser

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166          115          120          125
169 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu
170          130          135          140
173 Ser Val Thr Pro Gly Asp Gln Val Ser Leu Ser Cys Arg Ala Ser Gln
174 145          150          155          160
177 Ser Ile Ser Asp Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser
178          165          170          175
181 Pro Gln Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro
182          180          185          190
185 Ser Arg Phe Ser Gly Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile
186          195          200          205
189 Asn Ser Val Glu Pro Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly
190          210          215          220
193 His Ser Phe Pro Leu Thr Phe Gly Ala Gly Thr Glu Leu Glu Leu Glu
194 225          230          235          240
197 Gln Ala Ala
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 354
203 <212> TYPE: DNA
204 <213> ORGANISM: Mus musculus
206 <400> SEQUENCE: 4
207 caggtccaac tgcagcagtc tggggctgaa ctggttaaagc ctggggcttc agtgaaattg      60
209 tcctgcaagg cttctggcta caccttcaca aactatgata taaactgggt gaggcagagg      120
211 cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactcaatac      180
213 aatgagaagt tcaagggcaa ggccacactg actacagaca catcctccag cacagcctac      240
215 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagacagact      300
217 acggctacct ggtttgctta ctggggccaa gggaccacgg tcaccgtctc ctca          354
220 <210> SEQ ID NO: 5
221 <211> LENGTH: 321
222 <212> TYPE: DNA
223 <213> ORGANISM: Mus musculus
225 <400> SEQUENCE: 5
226 gacatcgagc tcaactcagtc tccaaccacc ctgtctgtga ctccaggaga tagagtctct      60
228 ctttcttgca gggccagcca gagtattagc gactacttac actggtacca acaaaaatca      120
230 catgagtctc caaggcttct catcaaatat gcttcccaat ccattctctgg gatcccctcc      180
232 aggttcagtg gcagtggatc agggtcagat ttactctca gtatcaacag tgtggaacct      240
234 gaagatgttg gagtgtatta ctgtcaaaat ggtcacagct ttccgctcac gttcggtgct      300
236 gggaccaagc tggagctgaa a          321
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 45
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Linker used to produce an 8H9 scFV.
247 <400> SEQUENCE: 6
248 gatggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcg          45
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 118
253 <212> TYPE: PRT

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254 <213> ORGANISM: Mus musculus
256 <400> SEQUENCE: 7
258 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
259 1 5 10 15
262 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
263 20 25 30
266 Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
267 35 40 45
270 Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
271 50 55 60
274 Lys Gly Lys Ala Thr Leu Thr Thr Asp Thr Ser Ser Thr Ala Tyr
275 65 70 75 80
278 Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
279 85 90 95
282 Ala Arg Gln Thr Thr Ala Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr
283 100 105 110
286 Thr Val Thr Val Ser Ser
287 115
290 <210> SEQ ID NO: 8
291 <211> LENGTH: 107
292 <212> TYPE: PRT
293 <213> ORGANISM: Mus musculus
295 <400> SEQUENCE: 8
297 Asp Ile Glu Leu Thr Gln Ser Pro Thr Thr Leu Ser Val Thr Pro Gly
298 1 5 10 15
301 Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr
302 20 25 30
305 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
306 35 40 45
309 Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
310 50 55 60
313 Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
314 65 70 75 80
317 Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Ser Phe Pro Leu
318 85 90 95
321 Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
322 100 105
325 <210> SEQ ID NO: 9
326 <211> LENGTH: 15
327 <212> TYPE: PRT
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Linker used to produce an 8H9 scFV.
333 <400> SEQUENCE: 9
335 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
336 1 5 10 15
339 <210> SEQ ID NO: 10
340 <211> LENGTH: 613
341 <212> TYPE: PRT

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Input Set : A:\Sequence Listing.txt

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342 <213> ORGANISM: Pseudomonas aeruginosa
344 <400> SEQUENCE: 10
346 Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
347 1 5 10 15
350 Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
351 20 25 30
354 Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
355 35 40 45
358 Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
359 50 55 60
362 Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
363 65 70 75 80
366 Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
367 85 90 95
370 Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
371 100 105 110
374 Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
375 115 120 125
378 Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
379 130 135 140
382 Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
383 145 150 155 160
386 Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
387 165 170 175
390 Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
391 180 185 190
394 Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
395 195 200 205
398 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
399 210 215 220
402 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
403 225 230 235 240
406 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
407 245 250 255
410 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
411 260 265 270
414 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
415 275 280 285
418 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
419 290 295 300
422 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
423 305 310 315 320
426 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
427 325 330 335
430 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
431 340 345 350
434 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
435 355 360 365
438 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp

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VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing.txt

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date